

codes for an enzyme selected from the group consisting of citrate synthase, a gene of *Pseudomonas aeruginosa* that codes for citrate synthase, and malate dehydrogenase;

- (b) the transformation of plant cells with the recombinant DNA molecule, and
- (c) the regeneration of transgenic plants starting from transformed cells, or of seeds from plants obtained from these transformed cells, for one or several generations, wherein the genetic information of these transformed cells includes the recombinant DNA molecule coding for enzymes that synthesizes organic acids.

Claim 17 (amended). The method according to claim 1, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

Claim 27 (amended). The method according to claim 1, wherein the promoter is a constitutive promoter.

Claim 37 (amended). The method according to claim 1, wherein the promoter is a root-specific promoter.

Claim 47 (amended). The method according to claim 1, wherein the promoter is a promoter inducible by stress caused by low phosphate availability.

Claim 57 (amended). The method according to claim 1, wherein the promoter is a promoter inducible by stress caused by low iron availability.

Claim 67 (amended). The method according to claim 1, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

Claim 74 (amended). A recombinant heterologous DNA molecule comprising one or more genes that code for enzymes that synthesize organic acids, said gene comprising a gene that codes for a gene selected from the group consisting of citrate synthase and malate dehydrogenase, functionally linked to a promoter sequence functional in plants, and to a transcription termination/polyadenylation sequence functional in plants.

Claim 93 (amended). Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 74, wherein the plant is a plant selected from the group consisting of Poaceae, Lileaceae, Leguminoseae, Solanaceae, Caricaceae, Cucurbitaceae, Triticum spp., Oryza sativa, Zea mays, Sorghum bicolor, Avena sativa, Saccharum officianarum, Solanum tuberosum, Lycopersicum esculentum, and Glycine max.

Claim 98 (amended). Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 74.

Claim 127 (amended). Use of transgenic plants according to claim 74 in soils containing phosphates in forms not available for plant nutrition.